

# SEQUENCE LISTING

<110> Shi, Jinrui  
Beach, Larry  
Wang, Hongyu  
Rafalski, Antoni J.  
Rebecca E. Cahoon

<120> Novel Inositol Polyphosphate Kinase  
Genes and Uses Thereof

<130> 1286

<150> US 60/261,465

<151> 2001-01-12

<160> 37

<170> FastSEQ for Windows Version 4.0

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Val Ala Gly His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp
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Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu
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His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala Val Pro
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Ala Arg Ile Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr Arg Leu
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Leu Pro Thr Glu Ala Gln Pro Gly Glu Pro His Pro His Leu Val Leu
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Asp Asp Leu Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp Ile Lys

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Lys Tyr Leu Ala Lys Asp Arg Gly Thr Thr Ser Val Leu Leu Gly Phe			
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Arg Val Leu Arg Pro Ser Arg Arg Pro Arg Gly Arg Arg Val Ala Asp			
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Ala Pro Ala Leu Arg Val Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala			
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Arg Ser Arg Arg Arg Cys Thr Glu Glu Lys Val Glu Ser Cys His Ser			
190	195	200	
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Cys Ala Ser Ser Arg His Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser			
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Thr Arg Arg Arg Phe Phe Trp Ala Met Met Leu Leu Gln Ser Gln Gln			
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Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr			

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Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly				
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Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp				
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Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Tyr Leu Ala Lys Asp				
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Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Leu Arg Pro Ser				
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Gly Tyr Gly His Arg Arg Arg Pro Pro Arg Ala Pro Ala Leu Arg Val				
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Ile Arg Leu Pro Thr Arg Gly Trp Thr Ala Arg Ser Arg Arg Arg Cys				
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Thr Glu Glu Lys Val Glu Ser Cys His Ser Cys Ala Ser Ser Arg His				
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Gly Trp Arg Ser Arg Leu Cys Ser Thr Ser Thr Arg Arg Arg Phe Phe				
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agc aag ccg ggc ccg ctc atc gac ggc tcc ggc ctc ttc tac aag ccg	154
Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro	
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ctc cag gcc ggc gac cgt ggg gag cac gag gtc gct ttc tat gag gcg	202
Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala	
	35 40 45 50
ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc cga gac acc ttc ttc	250
Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe	
	55 60 65
ccc cgg ttc cac ggc acg cga ctc ctc ccc acc gag gcg cag ccc ggg	298
Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly	
	70 75 80



50 55 60  
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
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Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly  
85 90 95  
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp  
100 105 110  
Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp  
115 120 125  
Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg  
130 135 140  
Val Val Val Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val  
145 150 155 160  
Lys Ala Met Asp Thr Val Gly Val Arg Arg Val Leu Arg Arg Tyr Val  
165 170 175  
Ser Ser Ala Cys Arg Arg Gly Asp Gly Leu Arg Ala Arg Gly Gly Gly  
180 185 190  
Val Arg Arg Lys Arg Trp Ser Leu Val Thr Ala Ala Arg Ala Gln Gly  
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210 215 220  
Ser Gly Leu  
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Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala Ser Ala  
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Ser Lys Pro Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro  
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ctc cag gcc ggc gac cgt ggg gag cac gag gtc gct ttc tat gag gcg 202  
Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr Glu Ala  
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Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr Phe Phe  
55 60 65  
ccc cgg ttc cac ggc acg cga ctc ctc ccc acc gag gcg cag ccc ggg 298  
Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly  
70 75 80

gag ccg cat ccg cac ctc gtc ctc gac gac ctc ctc gcg gga ttt gag	346
Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly Phe Glu	
85 90 95	
gcg ccc tgc gtc gca gac atc aag atc ggc gcc atc acg tgg cca ccg	394
Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp Pro Pro	
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agt tcg ccg gag ccc tac atc gcc aag tgc ctc gcc atg gac cgc ggg	442
Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp Arg Gly	
115 120 125 130	
acc acg agc gtt ctg ctc gga ttc cgc gtc tcc ggc gtc cga gtc gtc	490
Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg Val Val	
135 140 145	
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Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val Lys Ala	
150 155 160	
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Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val Ser Ser	
165 170 175	
gtt gcc gac gag ggg atg gac tgt gcg ctc gcc gcg gcg gtg tac gga	634
Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Ala Val Tyr Gly	
180 185 190	
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Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala Trp Phe	
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gag gag cag act ctg ttc cac ttc tac tcg gcg tcg att ctt ctg ggc	730
Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu Leu Gly	
215 220 225	
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Tyr Asp Ala Ala Val Ala Ala Gly Gly Gly Gly Gly Gly Val Thr	
230 235 240	
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Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly Val Ile	
245 250 255	
gac cac aac ttc ctg ggc ggg ctc tgc tgc ctg atc aag ttc gtt tct	874
Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe Val Ser	
260 265 270	
gac att gtt cca gag act cct cag acg cag cct ttg ggt cct tct taa	922
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Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr  
35 40 45  
Glu Ala Phe Ser Ala His Ala Val Pro Ala Arg Ile Arg Asp Thr  
50 55 60  
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
65 70 75 80  
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly  
85 90 95  
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp  
100 105 110  
Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Met Asp  
115 120 125  
Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg  
130 135 140  
Val Val Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val  
145 150 155 160  
Lys Ala Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val  
165 170 175  
Ser Ser Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Val  
180 185 190  
Tyr Gly Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala  
195 200 205  
Trp Phe Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu  
210 215 220  
Leu Gly Tyr Asp Ala Ala Val Ala Ala Gly Gly Gly Gly Gly  
225 230 235 240  
Val Thr Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly  
245 250 255  
Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe  
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57

105

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Ser	Lys	Leu	Gly	Pro	Leu	Ile	Asp	Gly	Ser	Gly	Leu	Phe	Tyr	Lys	Pro		
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ctc	cag	gcc	ggc	gac	cgt	ggg	gag	cac	gag	gtc	gcc	ttc	tat	gag	gcg		201
Leu	Gln	Ala	Gly	Asp	Arg	Gly	Glu	His	Glu	Val	Ala	Phe	Tyr	Glu	Ala		
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Phe	Ser	Ala	His	Ala	Ala	Val	Pro	Ala	Arg	Ile	Arg	Asp	Thr	Phe	Phe		
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ccc	cgg	ttc	cac	ggc	acg	cga	ctc	ctc	ccc	acc	gag	gcg	cag	ccc	ggg		297
Pro	Arg	Phe	His	Gly	Thr	Arg	Leu	Leu	Pro	Thr	Glu	Ala	Gln	Pro	Gly		
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gag	ccg	cat	cct	cac	ctc	gtc	ctc	gac	gac	ctc	ctc	gcg	ggg	ttt	cag		345
Glu	Pro	His	Pro	His	Leu	Val	Leu	Asp	Asp	Leu	Leu	Ala	Gly	Phe	Gln		
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gcg	ccc	tgc	gtc	gca	gac	atc	aag	atc	ggc	gcc	atc	acg	tgg	cca	ccg		393
Ala	Pro	Cys	Val	Ala	Asp	Ile	Lys	Ile	Gly	Ala	Ile	Thr	Trp	Pro	Pro		
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Ser	Ser	Pro	Glu	Pro	Tyr	Ile	Ala	Lys	Cys	Leu	Ala	Lys	Asp	Arg	Gly		
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Thr	Thr	Ser	Val	Leu	Leu	Gly	Phe	Arg	Val	Ser	Gly	Val	Arg	Val	Val		
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ggc	ccc	gag	ggc	gcc	gtg	tgg	cgg	acg	gag	cgc	ccg	gag	gtg	aag	gcc		537
Gly	Pro	Glu	Gly	Ala	Val	Trp	Arg	Thr	Glu	Arg	Pro	Glu	Val	Lys	Ala		
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atg	gac	acc	gcc	ggc	gtc	cgc	cgc	gtg	ctc	cgg	cgc	tac	gtg	tca	tcc		585
Met	Asp	Thr	Ala	Gly	Val	Arg	Arg	Val	Leu	Arg	Arg	Tyr	Val	Ser	Ser		
		165				170						175					
gtt	gcc	gac	gag	ggg	atg	gac	tgt	gcg	ctc	gcc	gcg	gcg	gtg	tac	gga		633
Val	Ala	Asp	Glu	Gly	Met	Asp	Cys	Ala	Leu	Ala	Ala	Ala	Val	Tyr	Gly		
	180					185				190							
gga	aaa	ggt	gga	gtc	ttg	tca	cag	ctg	cgc	gag	ctc	aag	gcg	tgg	ttc		681
Gly	Lys	Gly	Gly	Val	Leu	Ser	Gln	Leu	Arg	Glu	Leu	Lys	Ala	Trp	Phe		
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Glu	Glu	Gln	Thr	Leu	Phe	His	Phe	Tyr	Ser	Ala	Ser	Ile	Leu	Leu	Gly		
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tat	gat	gct	gct	gca	gtc	gca	gca	ggc	gga	gat	ggg	ggt	ggg	gtg	acg		777
Tyr	Asp	Ala	Ala	Ala	Val	Ala	Ala	Gly	Gly	Asp	Gly	Gly	Gly	Val	Thr		
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Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly Val Ile  
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gac cac aac ttc ctg ggc ggg ctc tgc tgc ctg atc aag ttc gtt tct 873  
Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe Val Ser  
260 265 270

gac att gtt ccg gag act cct cat acg cag cct ttg ggt cct tct taa 921  
Asp Ile Val Pro Glu Thr Pro His Thr Gln Pro Leu Gly Pro Ser \*  
275 280 285

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35 40 45  
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr  
50 55 60  
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln  
65 70 75 80  
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly  
85 90 95  
Phe Gln Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr Trp  
100 105 110  
Pro Pro Ser Ser Pro Glu Pro Tyr Ile Ala Lys Cys Leu Ala Lys Asp  
115 120 125  
Arg Gly Thr Thr Ser Val Leu Leu Gly Phe Arg Val Ser Gly Val Arg  
130 135 140  
Val Val Gly Pro Glu Gly Ala Val Trp Arg Thr Glu Arg Pro Glu Val  
145 150 155 160  
Lys Ala Met Asp Thr Ala Gly Val Arg Arg Val Leu Arg Arg Tyr Val  
165 170 175  
Ser Ser Val Ala Asp Glu Gly Met Asp Cys Ala Leu Ala Ala Val  
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Tyr Gly Gly Lys Gly Gly Val Leu Ser Gln Leu Arg Glu Leu Lys Ala  
195 200 205  
Trp Phe Glu Glu Gln Thr Leu Phe His Phe Tyr Ser Ala Ser Ile Leu  
210 215 220  
Leu Gly Tyr Asp Ala Ala Ala Val Ala Ala Gly Gly Asp Gly Gly Gly  
225 230 235 240

Val Thr Val Lys Leu Val Asp Phe Ala His Val Ala Glu Gly Asp Gly  
245 250 255  
Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu Ile Lys Phe  
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Ser

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Ala Lys Asp Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe  
15 20 25  
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Tyr Lys Pro Leu Gln Thr Asn Lys Asp Asp Asp Thr Arg Gly Ser Thr  
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gaa ctc tcc ttt tac acc tct ctc gcc gcc gcc gcc cac gac tac tcc 194  
Glu Leu Ser Phe Tyr Thr Ser Leu Ala Ala Ala Ala His Asp Tyr Ser  
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Ile Arg Ser Phe Phe Pro Ala Phe His Gly Thr Arg Leu Leu Asp Ala  
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Ser Asp Gly Ser Gly Pro His Pro His Leu Val Leu Glu Asp Leu Leu  
80 85 90  
tgc ggc tac tcc aaa ccc tcc gtc atg gac gta aag atc ggc tcc aga 338  
Cys Gly Tyr Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg  
95 100 105  
acc tgg cac ctg gga gac tcc gag gac tac atc tgc aag tgc ctg aag 386  
Thr Trp His Leu Gly Asp Ser Glu Asp Tyr Ile Cys Lys Cys Leu Lys  
110 115 120 125  
aag gac aga gag tcc tct agc ttg ccc ttg ggt ttc aga atc tcg gga 434  
Lys Asp Arg Glu Ser Ser Ser Leu Pro Leu Gly Phe Arg Ile Ser Gly  
130 135 140  
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Val Lys Asp Ser Ile Ser Ser Trp Glu Pro Thr Arg Lys Ser Leu Gln

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160	165	170	
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Ser Asn Asn Ile Asn His Asp Asp His His Pro Asp Cys Ala Phe Ala			
175	180	185	
acg gag gtc tac ggc gcc gtt ttg gag cgc ttg cag aag ctc aag gac			626
Thr Glu Val Tyr Gly Ala Val Leu Glu Arg Leu Gln Lys Leu Lys Asp			
190	195	200	205
tgg ttc gag gtt cag acg gtg tat cac ttc tat tct tgt tct gtt ctt			674
Trp Phe Glu Val Gln Thr Val Tyr His Phe Tyr Ser Cys Ser Val Leu			
210	215	220	
gtg gtg tac gag aag gat cta ggg aaa ggg aaa gct acc aac cct ctg			722
Val Val Tyr Glu Lys Asp Leu Gly Lys Gly Lys Ala Thr Asn Pro Leu			
225	230	235	
gtc aaa ctc gtt gac ttt gca cac gtg gtg gac gga aac ggt gtc att			770
Val Lys Leu Val Asp Phe Ala His Val Val Asp Gly Asn Gly Val Ile			
240	245	250	
gat cac aac ttc ttg ggt ggc ctt tgt tcc ttc atc aag ttc ctc aag			818
Asp His Asn Phe Leu Gly Gly Leu Cys Ser Phe Ile Lys Phe Leu Lys			
255	260	265	
gat atc cta gca gta gca tgt ctt cac aag tga ctgattttca tcgagttaat			871
Asp Ile Leu Ala Val Ala Cys Leu His Lys *			
270	275		
cttattccta tcagaaaata attatgcttg aattagtgtc gcagactaac tgtttgaagt			931
actgtcagaa acaaaataat aatatggact gagaggcaat cttgttctgc taaactccct			991
ttcaagttgc tgtcagatac tagccgtccc ttttcctttt tcatattctg tcaaagttag			1051
tcatttaata ataataacaa tgtccttcaa ctccaaaaaa aaaaaaaaaa aaaa			1105
<210> 10			
<211> 279			
<212> PRT			
<213> Glycine max			
<400> 10			
Met Leu Lys Ile Pro Glu His Gln Val Ala Gly His Lys Ala Lys Asp			
1 5 10 15			
Gly Ile Leu Gly Pro Leu Val Asp Asp Phe Gly Lys Phe Tyr Lys Pro			
20 25 30			
Leu Gln Thr Asn Lys Asp Asp Asp Thr Arg Gly Ser Thr Glu Leu Ser			
35 40 45			
Phe Tyr Thr Ser Leu Ala Ala Ala His Asp Tyr Ser Ile Arg Ser			
50 55 60			
Phe Phe Pro Ala Phe His Gly Thr Arg Leu Leu Asp Ala Ser Asp Gly			
65 70 75 80			
Ser Gly Pro His Pro His Leu Val Leu Glu Asp Leu Leu Cys Gly Tyr			
85 90 95			
Ser Lys Pro Ser Val Met Asp Val Lys Ile Gly Ser Arg Thr Trp His			

	100		105		110
Leu Gly Asp Ser Glu Asp Tyr Ile Cys Lys Cys Leu Lys Lys Asp Arg					
	115		120		125
Glu Ser Ser Ser Leu Pro Leu Gly Phe Arg Ile Ser Gly Val Lys Asp					
	130		135		140
Ser Ile Ser Ser Trp Glu Pro Thr Arg Lys Ser Leu Gln Cys Leu Ser					
145		150		155	160
Ala His Gly Val Ala Leu Val Leu Asn Lys Phe Val Ser Ser Asn Asn					
	165		170		175
Ile Asn His Asp Asp His His Pro Asp Cys Ala Phe Ala Thr Glu Val					
	180		185		190
Tyr Gly Ala Val Leu Glu Arg Leu Gln Lys Leu Lys Asp Trp Phe Glu					
	195		200		205
Val Gln Thr Val Tyr His Phe Tyr Ser Cys Ser Val Leu Val Val Tyr					
	210		215		220
Glu Lys Asp Leu Gly Lys Gly Lys Ala Thr Asn Pro Leu Val Lys Leu					
225		230		235	240
Val Asp Phe Ala His Val Val Asp Gly Asn Gly Val Ile Asp His Asn					
	245		250		255
Phe Leu Gly Gly Leu Cys Ser Phe Ile Lys Phe Leu Lys Asp Ile Leu					
	260		265		270
Ala Val Ala Cys Leu His Lys					
	275				

<210> 11  
 <211> 1195  
 <212> DNA  
 <213> Eucalyptus grandis

<220>  
 <221> CDS  
 <222> (116)...(1048)

<400> 11	
gcaccagctt cttggagtag ttgccatca gcgtggattt tcatttttagt ccattctggct	60
gtgatcaatc gaattctgagt aagtttggag aatttttttcg cacatcagat acacc atg	118
	Met
	1
ctc aag gtc ccg gat cat caa gtc gcc ggt cac cgg gga gac ggg gga	166
Leu Lys Val Pro Asp His Gln Val Ala Gly His Arg Gly Asp Gly Gly	
	5 10 15
aag ctg ggg cca ctg gtg gat gat tcg ggc cgc ttc tat aag cct ctc	214
Lys Leu Gly Pro Leu Val Asp Asp Ser Gly Arg Phe Tyr Lys Pro Leu	
	20 25 30
cag agc gat cat cgc gga gac acg gaa gtg gcc ttt tac gag tca ttc	262
Gln Ser Asp His Arg Gly Asp Thr Glu Val Ala Phe Tyr Glu Ser Phe	
	35 40 45
tat tcc aat acc gag atc cca ggt cac att cgc aaa ttc ttt cct gcg	310
Tyr Ser Asn Thr Glu Ile Pro Gly His Ile Arg Lys Phe Phe Pro Ala	
	50 55 60 65
ttt cac gga act aag act att gag gcg tct gat gga tcg ggt cct caa	358
Phe His Gly Thr Lys Thr Ile Glu Ala Ser Asp Gly Ser Gly Pro Gln	

70	75	80	
cct cac ctg gtt ctg gag gat ctc gtc tcg ggt cgc acg aac cca tct Pro His Leu Val Leu Glu Asp Leu Val Ser Gly Arg Thr Asn Pro Ser 85 90 95			406
ctc atg gac atc aag act gga tcc aga aca tgg tat ccg gag gcc tct Leu Met Asp Ile Lys Thr Gly Ser Arg Thr Trp Tyr Pro Glu Ala Ser 100 105 110			454
gag gag tac atc caa aag tgc tta gag aaa gat cga aat agc aca agc Glu Glu Tyr Ile Gln Lys Cys Leu Glu Lys Asp Arg Asn Ser Thr Ser 115 120 125			502
gtt tca ttg ggt ttt agg att tct ggg cta agg gta tat caa aat agc Val Ser Leu Gly Phe Arg Ile Ser Gly Leu Arg Val Tyr Gln Asn Ser 130 135 140 145			550
gaa gct gga ttt tgg caa cct gag aag aag gtt gtt tat agc ttt aat Glu Ala Gly Phe Trp Gln Pro Glu Lys Lys Val Val Tyr Ser Phe Asn 150 155 160			598
gcg gac ggt gtc agg tcg gct ctg agg aag ttt gtt tct tcc aac ttg Ala Asp Gly Val Arg Ser Ala Leu Arg Lys Phe Val Ser Ser Asn Leu 165 170 175			646
tct ctg ggt cca aat gtg gat ccg gat tgt ttg tat gca tca aaa gtt Ser Leu Gly Pro Asn Val Asp Pro Asp Cys Leu Tyr Ala Ser Lys Val 180 185 190			694
tac tgt cac cgg ggt gga att ttg gca caa ttg ctt cag ctg aag gaa Tyr Cys His Arg Gly Gly Ile Leu Ala Gln Leu Leu Gln Leu Lys Glu 195 200 205			742
tgg ttt gag gtt cag acg aat tat cac ttc tat tct tgt tca ctc att Trp Phe Glu Val Gln Thr Asn Tyr His Phe Tyr Ser Cys Ser Leu Ile 210 215 220 225			790
atc tta tat gac agg gag tct gct ttg gac ggc tgt gca cac ccg aaa Ile Leu Tyr Asp Arg Glu Ser Ala Leu Asp Gly Cys Ala His Pro Lys 230 235 240			838
gtt aaa ctg gtg gac ttt gca cat gtg atg gat ggc cac ggc gtg atc Val Lys Leu Val Asp Phe Ala His Val Met Asp Gly His Gly Val Ile 245 250 255			886
gat cac aac ttc ttg ggt ggc ctc tgt tct gta atc aag ttt ata cgt Asp His Asn Phe Leu Gly Gly Leu Cys Ser Val Ile Lys Phe Ile Arg 260 265 270			934
gac att gct gat gaa gat aac aag tgt gca aag tgc gaa gtc aat ctt Asp Ile Ala Asp Glu Asp Asn Lys Cys Ala Lys Cys Glu Val Asn Leu 275 280 285			982
gga ttg aaa gaa aat ggc ttc tat aag agc agc acg gaa cca gag ctt Gly Leu Lys Glu Asn Gly Phe Tyr Lys Ser Ser Thr Glu Pro Glu Leu 290 295 300 305			1030

gat cac gag gcc tgc tag tggaaactgg agaataactg cattcatgca 1078  
 Asp His Glu Ala Cys \*  
 310

ttcctgcatt cctgctctga caagtgggtc agaatgggta taataacagt ctatttttagt 1138  
 caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1195

<210> 12  
 <211> 310  
 <212> PRT  
 <213> Eucalyptus grandis

<400> 12  
 Met Leu Lys Val Pro Asp His Gln Val Ala Gly His Arg Gly Asp Gly  
 1 5 10 15  
 Gly Lys Leu Gly Pro Leu Val Asp Asp Ser Gly Arg Phe Tyr Lys Pro  
 20 25 30  
 Leu Gln Ser Asp His Arg Gly Asp Thr Glu Val Ala Phe Tyr Glu Ser  
 35 40 45  
 Phe Tyr Ser Asn Thr Glu Ile Pro Gly His Ile Arg Lys Phe Phe Pro  
 50 55 60  
 Ala Phe His Gly Thr Lys Thr Ile Glu Ala Ser Asp Gly Ser Gly Pro  
 65 70 75 80  
 Gln Pro His Leu Val Leu Glu Asp Leu Val Ser Gly Arg Thr Asn Pro  
 85 90 95  
 Ser Leu Met Asp Ile Lys Thr Gly Ser Arg Thr Trp Tyr Pro Glu Ala  
 100 105 110  
 Ser Glu Glu Tyr Ile Gln Lys Cys Leu Glu Lys Asp Arg Asn Ser Thr  
 115 120 125  
 Ser Val Ser Leu Gly Phe Arg Ile Ser Gly Leu Arg Val Tyr Gln Asn  
 130 135 140  
 Ser Glu Ala Gly Phe Trp Gln Pro Glu Lys Lys Val Val Tyr Ser Phe  
 145 150 155 160  
 Asn Ala Asp Gly Val Arg Ser Ala Leu Arg Lys Phe Val Ser Ser Asn  
 165 170 175  
 Leu Ser Leu Gly Pro Asn Val Asp Pro Asp Cys Leu Tyr Ala Ser Lys  
 180 185 190  
 Val Tyr Cys His Arg Gly Gly Ile Leu Ala Gln Leu Leu Gln Leu Lys  
 195 200 205  
 Glu Trp Phe Glu Val Gln Thr Asn Tyr His Phe Tyr Ser Cys Ser Leu  
 210 215 220  
 Ile Ile Leu Tyr Asp Arg Glu Ser Ala Leu Asp Gly Cys Ala His Pro  
 225 230 235 240  
 Lys Val Lys Leu Val Asp Phe Ala His Val Met Asp Gly His Gly Val  
 245 250 255  
 Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Val Ile Lys Phe Ile  
 260 265 270  
 Arg Asp Ile Ala Asp Glu Asp Asn Lys Cys Ala Lys Cys Glu Val Asn  
 275 280 285  
 Leu Gly Leu Lys Glu Asn Gly Phe Tyr Lys Ser Ser Thr Glu Pro Glu  
 290 295 300  
 Leu Asp His Glu Ala Cys  
 305 310

<210> 13  
 <211> 1020  
 <212> DNA

<213> Parthenium argentatum

<220>

<221> CDS

<222> (21) ... (908)

<400> 13

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gcacgagaac ttcttcagac atg ctc aag gcc cca gat cat cag gtt gct gga      53
                Met Leu Lys Ala Pro Asp His Gln Val Ala Gly
                  1                5                10

cat gaa gct ggg ctc ggg aag ctt ggc cca ctc att gat gat tca ggc      101
His Glu Ala Gly Leu Gly Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly
              15                20                25

cgg ttt tac aaa cca ctg cag ggt gat aac cgt ggg tca gaa gaa gta      149
Arg Phe Tyr Lys Pro Leu Gln Gly Asp Asn Arg Gly Ser Glu Glu Val
              30                35                40

gcc ttt tat gaa tca ttt tct tct aac aat aat att cca gaa cac ata      197
Ala Phe Tyr Glu Ser Phe Ser Ser Asn Asn Asn Ile Pro Glu His Ile
              45                50                55

cgc aaa ttc ttt cct ata tat tat ggc acc aaa atc atg aag gca tcc      245
Arg Lys Phe Phe Pro Ile Tyr Tyr Gly Thr Lys Ile Met Lys Ala Ser
              60                65                70                75

act ggc tct gac cat cct cac atg gtg ttg caa gat ctt aca tca gct      293
Thr Gly Ser Asp His Pro His Met Val Leu Gln Asp Leu Thr Ser Ala
              80                85                90

cat gtc aac cca tct gta atg gac atc aaa atc ggg tcc aga aca tgg      341
His Val Asn Pro Ser Val Met Asp Ile Lys Ile Gly Ser Arg Thr Trp
              95                100                105

gcg cca gaa gct tcc gag gcg tac att gca aaa tgc tta aaa aag gat      389
Ala Pro Glu Ala Ser Glu Ala Tyr Ile Ala Lys Cys Leu Lys Lys Asp
              110                115                120

agg gaa agc aca agt att cca ttg gga ttc agg atc tcc ggg ctg caa      437
Arg Glu Ser Thr Ser Ile Pro Leu Gly Phe Arg Ile Ser Gly Leu Gln
              125                130                135

gtc tat atc gat gat ggg tca ggg ttt tat aag cct cat aga aat tac      485
Val Tyr Ile Asp Asp Gly Ser Gly Phe Tyr Lys Pro His Arg Asn Tyr
              140                145                150                155

atg cgt aaa acc ggc cca gct gat gtt aga cta ctt ctt agg aaa ttt      533
Met Arg Lys Thr Gly Pro Ala Asp Val Arg Leu Leu Leu Arg Lys Phe
              160                165                170

gtt tct tct aac ccg tct gca gag atg gaa atg cgc aca ggc cta ggc      581
Val Ser Ser Asn Pro Ser Ala Glu Met Glu Met Arg Thr Gly Leu Gly
              175                180                185

ccg gat tgt tct tta gca tct ttt gtt tat ggt ggg cct aat ggg ata      629
Pro Asp Cys Ser Leu Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile
              190                195                200
```

tta gct caa ctg atg gaa ttg aag aca tgg ttt gaa gat caa aca att	677
Leu Ala Gln Leu Met Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile	
205 210 215	
tac cac ttc tat gct tgt tct ttt ttg ttc atc ttt gaa aag agg ttg	725
Tyr His Phe Tyr Ala Cys Ser Phe Leu Phe Ile Phe Glu Lys Arg Leu	
220 225 230 235	
gtg tta aaa ggt gct cgg tca aac gca gaa gtc aaa ctt att gat ttt	773
Val Leu Lys Gly Ala Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe	
240 245 250	
gct cat gtt aca gat ggt aat ggt gtt att gat cac aat ttc ttg ggt	821
Ala His Val Thr Asp Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly	
255 260 265	
ggg ctc tgt tct ttg ata aag ttc att tct gac ata ctt tcg gag aca	869
Gly Leu Cys Ser Leu Ile Lys Phe Ile Ser Asp Ile Leu Ser Glu Thr	
270 275 280	
aaa gat tgt aat ggt aca aac ggt cag gtt gaa ctt tga aactctcttc	918
Lys Asp Cys Asn Gly Thr Asn Gly Gln Val Glu Leu *	
285 290 295	
ttgttgcttt tcttcaataa tttatcatga cagtgtttaa ttgtaaagat attcgcttac	978
cggaatatat cttgggttatg agtgaaaaaa aaaaaaaaaa aa	1020

<210> 14  
 <211> 295  
 <212> PRT  
 <213> Parthenium argentatum

<400> 14

Met Leu Lys Ala Pro Asp His Gln Val Ala Gly His Glu Ala Gly Leu	
1 5 10 15	
Gly Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly Arg Phe Tyr Lys Pro	
20 25 30	
Leu Gln Gly Asp Asn Arg Gly Ser Glu Glu Val Ala Phe Tyr Glu Ser	
35 40 45	
Phe Ser Ser Asn Asn Asn Ile Pro Glu His Ile Arg Lys Phe Phe Pro	
50 55 60	
Ile Tyr Tyr Gly Thr Lys Ile Met Lys Ala Ser Thr Gly Ser Asp His	
65 70 75 80	
Pro His Met Val Leu Gln Asp Leu Thr Ser Ala His Val Asn Pro Ser	
85 90 95	
Val Met Asp Ile Lys Ile Gly Ser Arg Thr Trp Ala Pro Glu Ala Ser	
100 105 110	
Glu Ala Tyr Ile Ala Lys Cys Leu Lys Lys Asp Arg Glu Ser Thr Ser	
115 120 125	
Ile Pro Leu Gly Phe Arg Ile Ser Gly Leu Gln Val Tyr Ile Asp Asp	
130 135 140	
Gly Ser Gly Phe Tyr Lys Pro His Arg Asn Tyr Met Arg Lys Thr Gly	
145 150 155 160	
Pro Ala Asp Val Arg Leu Leu Leu Arg Lys Phe Val Ser Ser Asn Pro	
165 170 175	
Ser Ala Glu Met Glu Met Arg Thr Gly Leu Gly Pro Asp Cys Ser Leu	
180 185 190	



Ala Ser Phe Val Tyr Gly Gly Pro Asn Gly Ile Leu Ala Gln Leu Met  
 195 200 205  
 Glu Leu Lys Thr Trp Phe Glu Asp Gln Thr Ile Tyr His Phe Tyr Ala  
 210 215 220  
 Cys Ser Phe Leu Phe Ile Phe Glu Lys Arg Leu Val Leu Lys Gly Ala  
 225 230 235 240  
 Arg Ser Asn Ala Glu Val Lys Leu Ile Asp Phe Ala His Val Thr Asp  
 245 250 255  
 Gly Asn Gly Val Ile Asp His Asn Phe Leu Gly Gly Leu Cys Ser Leu  
 260 265 270  
 Ile Lys Phe Ile Ser Asp Ile Leu Ser Glu Thr Lys Asp Cys Asn Gly  
 275 280 285  
 Thr Asn Gly Gln Val Glu Leu  
 290 295

<210> 15  
 <211> 899  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (89)...(424)

<400> 15  
 gccccaaaat ctctttctcc gctgcgccgc aaaccaccg cttccaccat cgccaccggt 60  
 cacccttgc tcccatagtc cccatacc atg ccc gac ctc cac ccg ccg gag 112  
 Met Pro Asp Leu His Pro Pro Glu  
 1 5  
 cac caa gtc gcc ggt cac cgc gcc tcc gcc agc aag ctg ggc cca ctc 160  
 His Gln Val Ala Gly His Arg Ala Ser Ala Ser Lys Leu Gly Pro Leu  
 10 15 20  
 atc gac ggc tct ggc ctc ttc tac aag ccg ctc cag gcc ggc gac cgt 208  
 Ile Asp Gly Ser Gly Leu Phe Tyr Lys Pro Leu Gln Ala Gly Asp Arg  
 25 30 35 40  
 ggg gag cac gag gtc gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc 256  
 Gly Glu His Glu Val Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala  
 45 50 55  
 gtc ccg gcc cgc atc cga gac acc ttc ttc ccc ccg ttc cac ggc acg 304  
 Val Pro Ala Arg Ile Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr  
 60 65 70  
 cga ctc ctc ccc acc gag gcg cag ccc ggg gag ccg cat ccg tac ctc 352  
 Arg Leu Leu Pro Thr Glu Ala Gln Pro Gly Glu Pro His Pro Tyr Leu  
 75 80 85  
 gtc ctc gac gac ctc ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac 400  
 Val Leu Asp Asp Leu Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp  
 90 95 100  
 atc aag atc ggt gcc atc acg tga ccatgagcga tctgctcgga ttccacgtct 454  
 Ile Lys Ile Gly Ala Ile Thr \*  
 105 110

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ccggcgctccg agtcgtcggc cccgagggcg ccgtgtggcg gacggagcgc cctgaggtga 514
aggctatgga cattgtcggc gtccgccgcg tgctccggcg ctgcatgtca tccgcttgcc 574
ggcgagggga tggactgcgc gctcgcggcg gcggtgtacg gaggaaaagg tggagtcttg 634
tcacagctgc gcgagctcaa ggcgtgggtc gaggggcaga ctctgttcca cttctactcg 694
gcgtcgattc ttctgggcta tgatgctgct gcagtcgcag caggcggagg tgggggtggg 754
gtaacagtga agctgggtga ccttgcccat gtggccgagg gtgatggggg gattgaccac 814
aacttcctgg gcgggctctg ctactgtatc aagtttgttt ctgacattgt tccagagact 874
ccttagacgc agcaaggcg aattc 899

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<210> 16
<211> 111
<212> PRT
<213> Zea mays

```

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<400> 16
Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
 1           5           10           15
Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Gly Ser Gly Leu Phe Tyr
      20           25           30
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
      35           40           45
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
      50           55           60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
      65           70           75           80
Pro Gly Glu Pro His Pro Tyr Leu Val Leu Asp Asp Leu Leu Ala Gly
      85           90           95
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr
      100          105          110

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<210> 17
<211> 643
<212> DNA
<213> Zea mays

```

```

<220>
<221> misc_feature
<222> (1)...(643)
<223> n = A,T,C or G

```

```

<400> 17
ggccgtccct gnttttggtta accaccccgcc cccaaaatct ctttctccgc tgcgctgcaa 60
accacccgct tccaccatcg ccactcgtca ccccttgctc ccatagtccc cataccatgc 120
ccgacctcca cccgccggag caccaagtcg ccggtcacgc cgcctccgcc agcaagctgg 180
gcccgtcat cgacggctcc ggctctttct acaagccgct ccaggccggc gaccgtgggg 240
agcacgaggt cgccttctat gaggcgttct ccgcccacgc cgnctgcccg gcccgcattc 300
gagacacctt cttcccccggt ttccacggca cgcgactcct cccacccgag gcgcagcccg 360
gggagccgca tccgcacctc gtctctgacg acctctctgc ggggtttgag gcgccttgcg 420
tcgcagacat caagatcggc gccatcacgt ggccacogag ttgcgcggag ccctacatcg 480
ncaagtacct ngccaaggac cgcgggacca cgagcgttct gctcggattc cgcgtcttgc 540
gtccgagtcg tcggcccgga gggcgccgtg tggcggacgg agcgccccgg ggggtgaangc 600
tatggacacc cgtcggngnc cggcgngtgc ttcgngngct acg 643

```

```

<210> 18
<211> 519
<212> DNA

```

206070 "462400"

<213> Zea mays

<220>

<221> misc\_feature

<222> (1)...(519)

<223> n = A,T,C or G

<400> 18

ggtacggang	aaaangtggg	gtcttgtcac	agctgcgcga	gctcaangcg	tggttcgagg	60
ggcagactct	gttccacttc	tactcggcgt	cgattcttct	gggctatgat	gctgctgcag	120
tcgcagcagg	cggangtggg	ggtggggtaa	cagtgaagct	ggtggacttt	gccccatgtg	180
ccgaggggtga	tgggggtgatt	gaccacaact	tcctgggcgg	gctctgctan	ctgatcaagt	240
ttgtttctga	cattgttcca	gagactcctc	agacgcagcc	tttgggtcct	tcctaagaaa	300
agatcctggc	atttttcgatt	tgataacaaa	ggaancactt	tcagctgcca	aaaaaaaaanc	360
accagtgaag	atgaaaataa	cattattgag	gaaagtccg	atnataaccc	accanattna	420
aaaaaaaaaag	gtcccaaatt	tcgaaaatn	tggatcttaa	gaataatctc	ctgaaaacan	480
aattataaaa	cgtgaaaacc	ccggctncnt	catttacnc			519

<210> 19

<211> 353

<212> DNA

<213> Zea mays

<220>

<221> misc\_feature

<222> (1)...(353)

<223> n = A,T,C or G

<400> 19

ctcaaggcat	ggttggagga	gcagactctg	ttccacttct	actcggcgtc	gattcttctg	60
ggctatgatg	ctgctgcagt	cgancaggc	ggaggtgggg	gtggggtaac	agtgaagctg	120
gtggactttg	cccatgtggc	cgaggggtgat	gggggtgatt	tgaccacaac	ttcctgggcg	180
agctctgcta	gctgatcaag	ttcgttttct	tgacattggt	ccaganactc	cttagacgcc	240
agcctttggg	tccttcctta	aaaaaagatc	cctgacnttt	ttgatttgat	tacnaaggaa	300
acactttcca	cttgccnaaa	aaaaaagccc	ntgaggatta	aaaaattaac	ntt	353

<210> 20

<211> 3416

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (72)...(407)

<400> 20

ccacgcgtcc	ggcaaacc	ccgcttcac	catcgccacc	cgtcaccct	tgctcccata	60
gtccccatac	c	atg	ccc	gac	ctc	110
	Met	Pro	Asp	Leu	His	
	1			5		
					10	
cac	cgc	gcc	tcc	gcc	agc	158
His	Arg	Ala	Ser	Ala	Ser	
	15			20		
					25	
ctc	ttc	tac	aag	ccg	ctc	206
Leu	Phe	Tyr	Lys	Pro	Leu	
	30			35		
					40	
					45	

gcc ttc tat gag gcg ttc tcc gcc cac gcc gcc gtc ccg gcc cgc atc 254  
Ala Phe Tyr Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile  
50 55 60

cga gac acc ttc ttc ccc cgg ttc cac ggc acg cga ctc ctc ccc acc 302  
Arg Asp Thr Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr  
65 70 75

gag gcg cag ccc ggg gag ccg cat ccg cac ctc gtc ctc gac gac ctc 350  
Glu Ala Gln Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu  
80 85 90

ctc gcg ggg ttt gag gcg ccc tgc gtc gca gac atc aag atc ggt gcc 398  
Leu Ala Gly Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala  
95 100 105

atc acg tga ccacgagcgt tctgctcgga ttccgcgtct ccggcggtccg 447  
Ile Thr \*  
110

agtcgtcggc cccgagggcg ccgtgtggcg gacggagcgc ccggaggtga aggctatgga 507  
cattgtcggc gtccgcgcgc tgcctcggcg ctacgtgtca tccgcttgcc gacgagggga 567  
tggaactgcgc gctcgcggcg gcggtgtacg gaggaagagg tggagtcttg tcacagctgc 627  
gcgagctcaa ggcgtgggtc gaggggcaga ctctgttcca cttctactcg gcgtcgattc 687  
ttctgggcta tgatgctgct gcagtcgcag caggcggagg tgggggtggg gtaacagtga 747  
agctgggtgga ctttgcctat gtggccgagg gtgatgggtt gattgaccac aacttcctgg 807  
gcgggctctg ctagctgacg aagtttgttt ctgacattgt tccagagact cctcagacgc 867  
agcctttggg tccctcttaa gagaggatcc tggcattttc gatttgataa caaaggaagc 927  
actttcagct gcaaaaaaag aaagcagcag tgaggatgaa gatgacagta gtgaggaaag 987  
ttcggtgatg gagccaacaa aagttgaaga aaagaaggct ccaaaagtat cagaaaaatat 1047  
tggatctgag gatgaatctt ctgaagacaa gactgataaa gacagtgaag agcctcaggc 1107  
atgccatcat ttaacacctc aggcattgcca tcatttttgt ttcacaactc aaaagttaaag 1167  
gaaaacagta aaagtatgca ggcagtatga gggacacaca tagtttactg aaactccctt 1227  
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cgcgccctct ccgtcgcgcg gagatggcag caccagcagc tccgcgcct caacatccac 1827  
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atagttgtta aaagtcaaat ccttgcctgg ggccgagggc tgggaacttt caaaagcgga 2007  
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cggcggttgc gctactccaa cctgaatgtg gcaatctgct atgcagaggg catgccaact 2547  
aatgagatgc tctacttacc tacattatta ttacatccct ctgaagttgt atcttcagaa 2607  
gttcacattg acagtatttg cttcctcttg ccatacttac ccatcatggc ccatgggggtg 2667

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tctatcttat catgccatct tcaaagaatg gcatcatggt aacaaaaatg aatgagaaat 2727
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gctctatagc acttcttgcg aaaagtggga atctttctct aactgaatta atgttagaat 2847
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gatgtacatc acttcactaa tcatgaaatc tgtagaaggc gaaactacta gccatatatg 3327
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tgaattatca aaaaaaaaaa aaaaaaaaaa 3416

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<210> 21  
 <211> 111  
 <212> PRT  
 <213> Zea mays

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<400> 21
Met Pro Asp Leu His Pro Pro Glu His Gln Val Ala Gly His Arg Ala
 1          5          10          15
Ser Ala Ser Lys Leu Gly Pro Leu Ile Asp Asp Ser Gly Leu Phe Tyr
          20          25          30
Lys Pro Leu Gln Ala Gly Asp Arg Gly Glu His Glu Val Ala Phe Tyr
          35          40          45
Glu Ala Phe Ser Ala His Ala Ala Val Pro Ala Arg Ile Arg Asp Thr
          50          55          60
Phe Phe Pro Arg Phe His Gly Thr Arg Leu Leu Pro Thr Glu Ala Gln
65          70          75          80
Pro Gly Glu Pro His Pro His Leu Val Leu Asp Asp Leu Leu Ala Gly
          85          90          95
Phe Glu Ala Pro Cys Val Ala Asp Ile Lys Ile Gly Ala Ile Thr
          100          105          110

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<210> 22  
 <211> 1448  
 <212> DNA  
 <213> Parthenium argentatum

<220>  
 <221> CDS  
 <222> (52)...(1020)

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gcacgaggca cactcaatgg ctccgatgct cagaggccaa cggagggtac c atg ctg 57
                                     Met Leu
                                     1

cca gct cca gct gtt cct aat ggc acg ggt gct ccg ctt aag gac gaa 105
Pro Ala Pro Ala Val Pro Asn Gly Thr Gly Ala Pro Leu Lys Asp Glu
 5          10          15

cct tcc aac ccc gat cag gcg cag cac cag cct gac gag cgc gtt caa 153
Pro Ser Asn Pro Asp Gln Ala Gln His Gln Pro Asp Glu Arg Val Gln
20          25          30

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cac ttc atc ctt ctt gaa gac ctt act gct ggc atg aca agg cct tgt	201
His Phe Ile Leu Leu Glu Asp Leu Thr Ala Gly Met Thr Arg Pro Cys	
35 40 45 50	
gtc tta gac ttg aag atg ggt acg cgc cag tat ggt gtg gaa gcc gat	249
Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu Ala Asp	
55 60 65	
gag aag aaa cag cgg tct caa cgg cgc aag tgt cag atg acc acc agt	297
Glu Lys Lys Gln Arg Ser Gln Arg Arg Lys Cys Gln Met Thr Thr Ser	
70 75 80	
gct caa ctc ggc gtg cga gtc tgc ggt atg caa att tgg aac gcc aag	345
Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn Ala Lys	
85 90 95	
acc cag agc tac atc ttc gag gac aag tac ttc ggt cga gat ctg aaa	393
Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp Leu Lys	
100 105 110	
gca gga aaa gaa ttt cag gac gcg ctt aag cgc ttt ttt tgg gat ggg	441
Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp Asp Gly	
115 120 125 130	
acg agc tac aaa gca gca aac aga cac ata ccc gtc ata ttg gag aag	489
Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu Glu Lys	
135 140 145	
atc agc caa ctg gaa cgc atg ata cga aaa ctt cca gga tac aga ttc	537
Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr Arg Phe	
150 155 160	
tac gcg agt agt ttg ttg atg ctc tat gat cgt ggg gac ggt gag tcg	585
Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly Glu Ser	
165 170 175	
aag gag aaa gac gca gca ccc tct tta cct aac ggc ttg tcg aac ccg	633
Lys Glu Lys Asp Ala Ala Pro Ser Leu Pro Asn Gly Leu Ser Asn Pro	
180 185 190	
agc aac gaa gac gtt tca aca ata cca tct gga ctt aca tca cca ggg	681
Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser Pro Gly	
195 200 205 210	
ccg aca gtc gct tct aaa ccg tca ccc aag aag cac gga gag atc aag	729
Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu Ile Lys	
215 220 225	
ctg aaa att gtc gac ttt gcc aac tgc gtg act gca gaa gac cct cta	777
Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp Pro Leu	
230 235 240	
cca gac gac tta cct tgt cca cct gaa aat ccc gac ggc atc gat aga	825
Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile Asp Arg	
245 250 255	
ggg tac ctc cgt ggc ctc cga tca cta cgc ctc tac ttc caa cgc att	873
Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln Arg Ile	

260 265 270

tgg aat gac atc aac gag gaa tgg gtc gaa cga ggc gag ggc gag ggc 921  
 Trp Asn Asp Ile Asn Glu Glu Trp Val Glu Arg Gly Glu Gly Glu Gly  
 275 280 285 290

atg gcg cga aat cat cac cat ggc cct ggt tta ggt gag gtt ggt gcg 969  
 Met Ala Arg Asn His His His Gly Pro Gly Leu Gly Glu Val Gly Ala  
 295 300 305

ggc tgg atg gat gat gct ggt ggt gag gat aca ggc tac gcc agt ttc 1017  
 Gly Trp Met Asp Asp Ala Gly Gly Glu Asp Thr Gly Tyr Ala Ser Phe  
 310 315 320

taa agaagaggag gaacagcaaa gctgcccacg ctcgacagaa gtcggacagt 1070  
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cgatattgat acgtccatcc cttttccctt cccttcattt ccacgttcag tctatttcac 1130  
 attgtgtgca ttttggttg caagcatggt gttttggtgc ataatggtaa gacaaaggt 1190  
 aatgaaattg gcaactcttt tggcatgcat cggcgagca ttttatgggc ggtcagaacc 1250  
 tctgcgttgt ggcttttagt ttttgaaatt tgcggaatct ggggtgttct tgaggcggat 1310  
 tctttgtata ttatcataaa gagtaggta gcgctagctc attaatacaa cactttgaat 1370  
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 aaaaaaaaaa aaaaaaaaaa 1448

<210> 23  
 <211> 322  
 <212> PRT  
 <213> Parthenium argentatum

<400> 23  
 Met Leu Pro Ala Pro Ala Val Pro Asn Gly Thr Gly Ala Pro Leu Lys  
 1 5 10 15  
 Asp Glu Pro Ser Asn Pro Asp Gln Ala Gln His Gln Pro Asp Glu Arg  
 20 25 30  
 Val Gln His Phe Ile Leu Leu Glu Asp Leu Thr Ala Gly Met Thr Arg  
 35 40 45  
 Pro Cys Val Leu Asp Leu Lys Met Gly Thr Arg Gln Tyr Gly Val Glu  
 50 55 60  
 Ala Asp Glu Lys Lys Gln Arg Ser Gln Arg Arg Lys Cys Gln Met Thr  
 65 70 75 80  
 Thr Ser Ala Gln Leu Gly Val Arg Val Cys Gly Met Gln Ile Trp Asn  
 85 90 95  
 Ala Lys Thr Gln Ser Tyr Ile Phe Glu Asp Lys Tyr Phe Gly Arg Asp  
 100 105 110  
 Leu Lys Ala Gly Lys Glu Phe Gln Asp Ala Leu Lys Arg Phe Phe Trp  
 115 120 125  
 Asp Gly Thr Ser Tyr Lys Ala Ala Asn Arg His Ile Pro Val Ile Leu  
 130 135 140  
 Glu Lys Ile Ser Gln Leu Glu Arg Met Ile Arg Lys Leu Pro Gly Tyr  
 145 150 155 160  
 Arg Phe Tyr Ala Ser Ser Leu Leu Met Leu Tyr Asp Arg Gly Asp Gly  
 165 170 175  
 Glu Ser Lys Glu Lys Asp Ala Ala Pro Ser Leu Pro Asn Gly Leu Ser  
 180 185 190  
 Asn Pro Ser Asn Glu Asp Val Ser Thr Ile Pro Ser Gly Leu Thr Ser  
 195 200 205

Pro Gly Pro Thr Val Ala Ser Lys Pro Ser Pro Lys Lys His Gly Glu  
 210 215 220  
 Ile Lys Leu Lys Ile Val Asp Phe Ala Asn Cys Val Thr Ala Glu Asp  
 225 230 235 240  
 Pro Leu Pro Asp Asp Leu Pro Cys Pro Pro Glu Asn Pro Asp Gly Ile  
 245 250 255  
 Asp Arg Gly Tyr Leu Arg Gly Leu Arg Ser Leu Arg Leu Tyr Phe Gln  
 260 265 270  
 Arg Ile Trp Asn Asp Ile Asn Glu Glu Trp Val Glu Arg Gly Glu Gly  
 275 280 285  
 Glu Gly Met Ala Arg Asn His His His Gly Pro Gly Leu Gly Glu Val  
 290 295 300  
 Gly Ala Gly Trp Met Asp Asp Ala Gly Gly Glu Asp Thr Gly Tyr Ala  
 305 310 315 320  
 Ser Phe

<210> 24  
 <211> 2270  
 <212> DNA  
 <213> Zea mays

<220>  
 <221> CDS  
 <222> (3)...(953)

<400> 24  
 cc acg cgt ccg cga aaa ttg aga aac att gtt cag tgg acg ccg ttc 47  
 Thr Arg Pro Arg Lys Leu Arg Asn Ile Val Gln Trp Thr Pro Phe  
 1 5 10 15  
 ttt caa act tac aaa aaa cag agg tat cca tgg gta cag cta gcc gga 95  
 Phe Gln Thr Tyr Lys Lys Gln Arg Tyr Pro Trp Val Gln Leu Ala Gly  
 20 25 30  
 cac caa ggc aat ttc aaa gcc ggt ccg gaa cct ggt acg atc ctc aag 143  
 His Gln Gly Asn Phe Lys Ala Gly Pro Glu Pro Gly Thr Ile Leu Lys  
 35 40 45  
 aaa ctt tgt ccc aaa gaa cag ttg tgc ttc caa gtg ctg atg aag gac 191  
 Lys Leu Cys Pro Lys Glu Gln Leu Cys Phe Gln Val Leu Met Lys Asp  
 50 55 60  
 gtt ctg aga ccg tac gtg ccc gaa tac aag ggc cac ttg act acc gac 239  
 Val Leu Arg Pro Tyr Val Pro Glu Tyr Lys Gly His Leu Thr Thr Asp  
 65 70 75  
 gac gga gac cta tat ctt cag cta gaa gac ttg ttg ggt gac ttc act 287  
 Asp Gly Asp Leu Tyr Leu Gln Leu Glu Asp Leu Leu Gly Asp Phe Thr  
 80 85 90 95  
 tcg ccg tgc gtc atg gac tgc aag atc ggc gtc agg acg tat ctg gaa 335  
 Ser Pro Cys Val Met Asp Cys Lys Ile Gly Val Arg Thr Tyr Leu Glu  
 100 105 110  
 gag gaa ctg gcg aaa gcc aaa gag aaa ccc aag ttg aga aaa gac atg 383  
 Glu Glu Leu Ala Lys Ala Lys Glu Lys Pro Lys Leu Arg Lys Asp Met



115	120	125	
tac gaa aaa atg att cag ata gac ccc aac gca cca tcg gag gag gaa			431
Tyr Glu Lys Met Ile Gln Ile Asp Pro Asn Ala Pro Ser Glu Glu Glu			
130	135	140	
cac cga ctg aag ggt gtg aca aaa ccg agg tac atg gtt tgg agg gag			479
His Arg Leu Lys Gly Val Thr Lys Pro Arg Tyr Met Val Trp Arg Glu			
145	150	155	
acg att tcg tcc acg gcc acg ttg ggc ttc cgg atc gag ggg atc aag			527
Thr Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys			
160	165	170	175
aaa agc gat gga aaa tcg agc aag gac ttc aag acg aca aag aac cgg			575
Lys Ser Asp Gly Lys Ser Ser Lys Asp Phe Lys Thr Thr Lys Asn Arg			
180	185	190	
gac cag gtg atc gaa gcg ttt cga gat ttc gtc gcc ggt ttc ccg cac			623
Asp Gln Val Ile Glu Ala Phe Arg Asp Phe Val Ala Gly Phe Pro His			
195	200	205	
gta atc ccc aag tac ata aac cga ctg aga gcg atc aga gac ata ctg			671
Val Ile Pro Lys Tyr Ile Asn Arg Leu Arg Ala Ile Arg Asp Ile Leu			
210	215	220	
gtg aac tcc aag ttt ttc act acg cac gag gtg atc ggc agc tcg ctg			719
Val Asn Ser Lys Phe Phe Thr Thr His Glu Val Ile Gly Ser Ser Leu			
225	230	235	
ctg ttc gtg cac gac agc aag aac gcc aac ata tgg ctt atc gac ttc			767
Leu Phe Val His Asp Ser Lys Asn Ala Asn Ile Trp Leu Ile Asp Phe			
240	245	250	255
gca aag acg ctc ata ctt ccg ccg gac atc cgg atc aac cac acg tcc			815
Ala Lys Thr Leu Ile Leu Pro Pro Asp Ile Arg Ile Asn His Thr Ser			
260	265	270	
gag tgg gtg gtg ggc aac cac gag gac ggt tac ctg atc ggt atc aac			863
Glu Trp Val Val Gly Asn His Glu Asp Gly Tyr Leu Ile Gly Ile Asn			
275	280	285	
aac ctg ctg gac ata ttc acc gat atg aac gcc gcc acc gcg ttt ccc			911
Asn Leu Leu Asp Ile Phe Thr Asp Met Asn Ala Ala Thr Ala Phe Pro			
290	295	300	
gtc acg ctc atc gaa gtc acg gcc ccg tcc gaa gtc acc tga			953
Val Thr Leu Ile Glu Val Thr Ala Pro Ser Glu Val Thr *			
305	310	315	
acgccgtcga tccccgccg taccctgact cgctcggcga cccactcgcc ggtgtcattc			1013
gattccagcc acccactcag tgggtcttgcg aatcacgtga cccaccccggt tgacaatgtg			1073
tgataataat aatatgtctg gcgcaaaaata ttccaaaaaag tctttttttaa attacacttt			1133
cgatttttcga cgacaaaacaa aatgacgcgcg ttttcggtac ctacctactg taggggttcgt			1193
tccgatttgcga atcataattt attttacccc caccacaacc cgaaccggt tatggccac			1253
cagaggattt gccatcagta ttaaaacaat gatctattat agatgtttaa aaataaatat			1313
tatataatta tacatcatcg cgggtgtgttg tgtaatatgc ctattataat atgtactata			1373
ttatacacat agcatattat aaaaatagta tattattata ttatattata ataattattat			1433

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ggttatgtgt gtttgtgtgg aaatccaata atataaaata atagttatta tttttaaata 1493
ctgtgtacgat aatgggacta ctacgtgtga ttctcaaagt atatatatat attaataattt 1553
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aattactata ctgtgcgtgc gataacataa taattttgta cctaatacat caatcaatta 1673
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aatacctatc cacgttacaa cgacaataat aataacaata atagtacctt tactttattt 1913
ttatttcctc acgaaaacga gaagtcctca tttctttctc ccgttacagt gtgtgtgtgt 1973
gtgtgtgtgt gtgtgtgtgt gtgtgtgtgt gcgtatgtgt atgtgtgaaa tttttgattt 2033
aattatatat tattataatt ttttctcctt atatttttat ttattattat aacatttttt 2093
ttgtgtgtac agaattttta aataagactt gtaaaagaaa cccttgttat attattttat 2153
tttttatttc acttcgcaca tgtgtacata ataaatcggt atcgccctta aaaaaaaaaa 2213
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaa 2270

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<210> 25  
 <211> 316  
 <212> PRT  
 <213> Zea mays

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<400> 25
Thr Arg Pro Arg Lys Leu Arg Asn Ile Val Gln Trp Thr Pro Phe Phe
 1          5          10          15
Gln Thr Tyr Lys Lys Gln Arg Tyr Pro Trp Val Gln Leu Ala Gly His
          20          25          30
Gln Gly Asn Phe Lys Ala Gly Pro Glu Pro Gly Thr Ile Leu Lys Lys
          35          40          45
Leu Cys Pro Lys Glu Gln Leu Cys Phe Gln Val Leu Met Lys Asp Val
          50          55          60
Leu Arg Pro Tyr Val Pro Glu Tyr Lys Gly His Leu Thr Thr Asp Asp
65          70          75          80
Gly Asp Leu Tyr Leu Gln Leu Glu Asp Leu Leu Gly Asp Phe Thr Ser
          85          90          95
Pro Cys Val Met Asp Cys Lys Ile Gly Val Arg Thr Tyr Leu Glu Glu
          100          105          110
Glu Leu Ala Lys Ala Lys Glu Lys Pro Lys Leu Arg Lys Asp Met Tyr
          115          120          125
Glu Lys Met Ile Gln Ile Asp Pro Asn Ala Pro Ser Glu Glu Glu His
          130          135          140
Arg Leu Lys Gly Val Thr Lys Pro Arg Tyr Met Val Trp Arg Glu Thr
145          150          155          160
Ile Ser Ser Thr Ala Thr Leu Gly Phe Arg Ile Glu Gly Ile Lys Lys
          165          170          175
Ser Asp Gly Lys Ser Ser Lys Asp Phe Lys Thr Thr Lys Asn Arg Asp
          180          185          190
Gln Val Ile Glu Ala Phe Arg Asp Phe Val Ala Gly Phe Pro His Val
          195          200          205
Ile Pro Lys Tyr Ile Asn Arg Leu Arg Ala Ile Arg Asp Ile Leu Val
210          215          220
Asn Ser Lys Phe Phe Thr His Glu Val Ile Gly Ser Ser Leu Leu
225          230          235          240
Phe Val His Asp Ser Lys Asn Ala Asn Ile Trp Leu Ile Asp Phe Ala
          245          250          255
Lys Thr Leu Ile Leu Pro Pro Asp Ile Arg Ile Asn His Thr Ser Glu
          260          265          270
Trp Val Val Gly Asn His Glu Asp Gly Tyr Leu Ile Gly Ile Asn Asn
          275          280          285
Leu Leu Asp Ile Phe Thr Asp Met Asn Ala Ala Thr Ala Phe Pro Val

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290                      295                      300  
 Thr Leu Ile Glu Val Thr Ala Pro Ser Glu Val Thr  
 305                      310                      315

<210> 26  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <222> (1)...(25)

<400> 26  
 accgcttcca ccatcgccac tcgtc 25

<210> 27  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <222> (1)...(30)

<400> 27  
 ccttagacgc agcctttggg tccttcttaa 30

<210> 28  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <221> primer\_bind  
 <222> (1)...(36)

<400> 28  
 tcgacccacg cgtccgaaaa aaaaaaaaaa aaaaaa 36

<210> 29  
 <211> 21  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> consensus sequence

<400> 29  
 Ile Leu Leu Glu Asn Leu Thr Ser Arg Tyr Glu Val Pro Cys Val Leu  
 1                      5                      10                      15  
 Asp Leu Lys Met Gly  
 20

<210> 30  
 <211> 33

<212> PRT  
<213> Artificial Sequence

<220>  
<223> consensus sequence

<221> VARIANT  
<222> (1)...(33)  
<223> Xaa = Any Amino Acid

<400> 30  
Leu Lys Xaa Pro Glu His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly  
1 5 10 15  
Lys Xaa Gly Pro Leu Val Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu  
20 25 30  
Gln

<210> 31  
<211> 33  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> consensus sequence

<221> VARIANT  
<222> (1)...(33)  
<223> Xaa = Any Amino Acid

<400> 31  
Leu Lys Xaa Pro Glu His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly  
1 5 10 15  
Lys Xaa Gly Pro Leu Ile Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu  
20 25 30  
Gln

<210> 32  
<211> 33  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> consensus sequence

<221> VARIANT  
<222> (1)...(33)  
<223> Xaa = Any Amino Acid

<400> 32  
Leu Lys Xaa Pro Asp His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly  
1 5 10 15  
Lys Xaa Gly Pro Leu Val Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu  
20 25 30  
Gln

<210> 33  
 <211> 33  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> consensus sequence

<221> VARIANT  
 <222> (1)...(33)  
 <223> Xaa = Any Amino Acid

<400> 33  
 Leu Lys Xaa Pro Asp His Gln Val Ala Gly His Xaa Ala Xaa Xaa Gly  
 1 5 10 15  
 Lys Xaa Gly Pro Leu Ile Asp Asp Xaa Gly Xaa Phe Tyr Lys Pro Leu  
 20 25 30  
 Gln

<210> 34  
 <211> 41  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> consensus sequence  
 <221> VARIANT  
 <222> (1)...(41)  
 <223> Xaa = Any Amino Acid

<400> 34  
 Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Ser Val Met Asp  
 1 5 10 15  
 Val Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr  
 20 25 30  
 Ile Xaa Lys Cys Leu Xaa Lys Asp Arg  
 35 40

<210> 35  
 <211> 41  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> consensus sequence  
 <221> VARIANT  
 <222> (1)...(41)  
 <223> Xaa = Any Amino Acid

<400> 35

Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Ser Val Met Asp  
 1 5 10 15  
 Ile Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr  
 20 25 30  
 Ile Xaa Lys Cys Leu Xaa Lys Asp Arg  
 35 40

<210> 36  
 <211> 41  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> consensus sequence

<221> VARIANT  
 <222> (1)...(41)  
 <223> Xaa = Any Amino Acid

<400> 36  
 Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Cys Val Met Asp  
 1 5 10 15  
 Val Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr  
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 Ile Xaa Lys Cys Leu Xaa Lys Asp Arg  
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<220>  
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<221> VARIANT  
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 Val Leu Xaa Asp Leu Xaa Xaa Xaa Xaa Xaa Xaa Pro Cys Val Met Asp  
 1 5 10 15  
 Ile Lys Xaa Gly Ser Arg Thr Trp Xaa Xaa Xaa Xaa Xaa Glu Xaa Tyr  
 20 25 30  
 Ile Xaa Lys Cys Leu Xaa Lys Asp Arg  
 35 40